AMENDMENT OF THE CLAIMS

Please amend the claims as follows. Language to be added is shown with an underline, and language to be deleted is shown with a strikethrough. This listing of claims will replace all prior versions and listings of claims in the application.

1. (Currently amended) A method for determining whether a human immunodeficiency virus type 1 virus (HIV-1) has an increased likelihood of having a reduced susceptibility to treatment with amprenavir, comprising:

detecting ~~whether the protease encoded by said HIV-1 exhibits~~ the presence or absence of a mutation in a protease associated with reduced susceptibility to treatment with amprenavir ~~said protease inhibitor~~ at amino acid position 11, 34, 47, 50, 76, 83, 91 or 95 of an amino acid sequence of said protease, wherein the mutation at amino acid position 34 is Q, ~~and wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having reduced susceptibility to treatment with amprenavir~~, with the proviso that said mutation is not I47V ~~I47V,~~ or I50V, and

determining whether the HIV-1 has an increased likelihood of having a reduced susceptibility to treatment with amprenavir, wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having a reduced susceptibility to treatment with amprenavir, and wherein the level of susceptibility, mutations, and position number are compared to the protease sequence of the NL4-3 reference strain.

2.-11. (Canceled)

12. (Previously presented) The method of claim 1, wherein the amino acid at position 11, 76, 91 or 95 of said protease is an amino acid having a neutral, hydrophobic or non-polar side chain.

13. (Original) The method of claim 12, wherein the amino acid at position 11 of said protease is I or L.

14.-20. (Canceled)

21. (Original) The method of claim 12, wherein the amino acid at position 76 of said protease is V.

22.-23. (Canceled)

24. (Original) The method of claim 12, wherein the amino acid at position 91 of said protease is A or V.

25. (Original) The method of claim 12, wherein the amino acid at position 95 of said protease is F.

26.-28. (Canceled)

29. (Previously presented) The method of claim 1, wherein the amino acid at position 83 of said protease is an amino acid with an acidic, hydrophilic or polar side chain.

30. (Canceled)

31. (Original) The method of claim 1, wherein the amino acid at position 83 of said protease is D.

32.-38. (Canceled)

39. (Original) The method of claim 1, wherein the amino acid at position 91 of said protease is an amino acid with a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.

40. (Original) The method of claim 1, wherein the amino acid at position 91 of said protease is an amino acid with a neutral, hydrophilic or polar side chain.

41. (Original) The method of claim 40, wherein the amino acid at position 91 of said protease is S.

42. (Currently amended) The method of claim 1, wherein the method comprises detecting the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at each one of at least 2, 3, 4, 5, 6, 7 or 8 ~~7, or 8,~~ of the amino acid positions.

43. (Currently amended) The method of claim 1, further comprising detecting the presence or absence ~~at least one~~ of a mutation in at least one ~~of an~~ amino acid position selected from the group consisting of position ~~at~~ 32, 33, 43, 46, 48, 54, 58, 71, 79, 82, and ~~or~~ 84, wherein the presence of said mutation indicates that the HIV-1 has an increased likelihood of having reduced susceptibility to treatment with amprenavir, with the proviso that the mutation is not V32I, M46I, M46L, I54L, I54M, or I84V, and wherein the level of susceptibility, mutations, and position number are compared ~~compare~~ to the protease sequence of the NL4-3 reference strain.

44. (Previously presented) The method of claim 43, wherein the amino acid at position 33, 43, 48, 54, 71, 82 or 84 of said protease is an amino acid having a neutral, hydrophobic or non-polar side chain.

45. (Previously presented) The method of claim 44, wherein the amino acid at position 33 of said protease is F.

46. (Previously presented) The method of claim 44, wherein the amino acid at position 48 of said protease is M.

47. (Previously presented) The method of claim 44, wherein the amino acid at position 54 of said protease is A.

48. (Previously presented) The method of claim 44, wherein the amino acid at position 71 of said protease is L.

49. (Previously presented) The method of claim 44, wherein the amino acid at position 82 of said protease is A or F.

50. (Previously presented) The method of claim 44, wherein the amino acid at position 84 of said protease is A.

51. (Previously presented) The method of claim 44, wherein the amino acid at position 43 of said protease is T.

52. (Previously presented) The method of claim 43, wherein the amino acid at position 54 of said protease is an amino acid having a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.

53. (Previously presented) The method of claim 52, wherein the amino acid at position 54 of said protease is S or T.

54. (Previously presented) The method of claim 43, wherein the amino acid at position 58 of said protease is an amino acid having an acidic, hydrophilic or polar side chain.

55. (Previously presented) The method of claim 54, wherein the amino acid at position 58 of said protease is E.

56. (Previously presented) The method of claim 43, wherein the amino acid at position 79 of said protease is an amino acid having a neutral, hydrophobic, non-polar, acidic, hydrophilic or polar side chain.

57. (Previously presented) The method of claim 56, wherein the amino acid at position 79 of said protease is not P.

58. (Previously presented) The method of claim 43, wherein the amino acid at position 84 of said protease is an amino acid having a neutral, hydrophobic, non-polar, hydrophilic or polar side chain.

59. (Previously presented) The method of claim 58, wherein the amino acid at position 84 of said protease is C.

60. (Currently amended) The method of claim 43, wherein the method comprises detecting the presence or absence of a mutation associated with reduced susceptibility to treatment with said protease inhibitor at each one of at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 of the amino acid positions.